

FIG. 1A

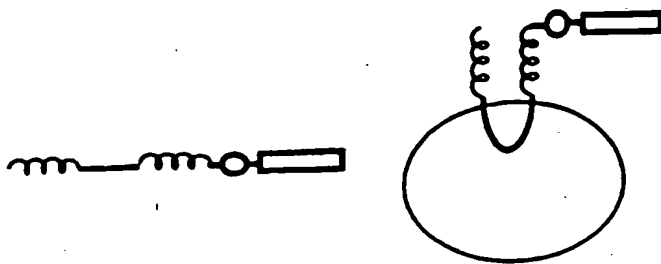


FIG. 1B

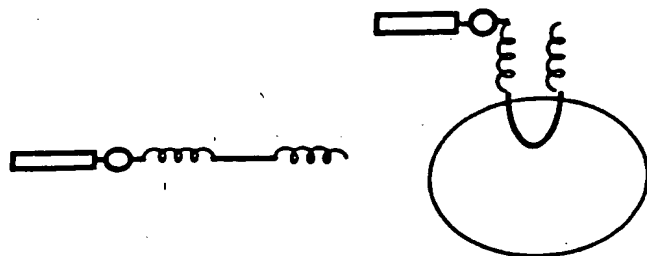


FIG. 1C

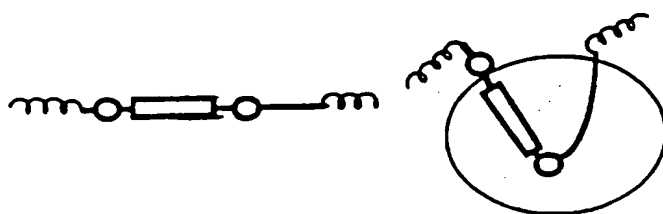


FIG. 1D

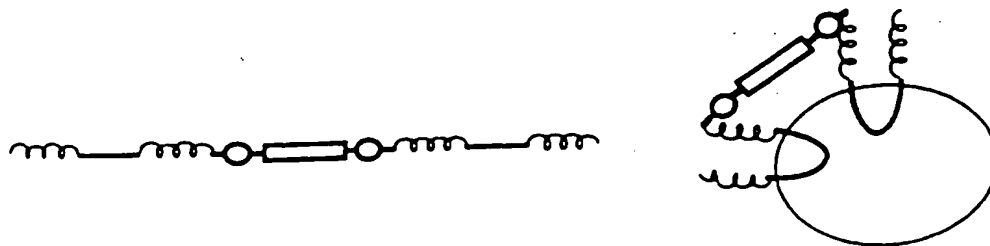


FIGURE 2

-067 ^{NcoI} CCAATGGCTATACCCAACTCGGTCTTGGTCAACACGGAACCTCTCTGGTAAAGCTAGCTCCACTCCCCAGAAACACGGCCGCAAAATTCG
 -177 CGGAATTGCTGACCTGAAGACGGAACATCATCGTCCGGTCCCTTGGGCGATTGCGGCGGAAGATGCGGTCAAGCTTGGGCTTGAGGACGAGAC
 -687 CGGAATCGAGTCTGTTGAAAGGTTGTTCAATTGGGATTGTATACGGAGATTGGTCTGTCGAGAGGTTTGAGGGAAAGGACAAATGGGTTTG
 R1
 -597 GCTCTGGAGAAAGAGAGTGGCGCTTTAGAGAGAGAGATTGAGAGGTTTAGAGAGAGAGATGCGGCGCGGATGACGGGAGGAGAGACGACGAGG
 R2 R2
 -507 ACCTGCATTATCAAAGCAGTGACGTGGTGAATTTGGAACCTTTTAGAGGCGAGATAGATTTATTATTGTATCCATTTTCTTCATTGTTTC
 R1
 -417 TAGAATGTCCGGGAACAAATTTTAAACTAAATCCTAAATTTTCTAAATTTGTTGCCAATAGTGGATATGTGGGCGGTATAGAAGGAAT
 -127 CTATTGAAGGCCCAACCCATACTGACGAGGCCAAAGGTTGCTTTTGGCTTTTATGTTTGGGTTGATGCCAACGCCACATTCCTGAGCTA
 I
 -237 GGCAAAAAACAAAGTGTCTTTGAATAGACTCCTCTCGTTAACACATGACAGCGGCTGCATGGTGACGCCATTAAACAGTGGGCTACAAAT
 -147 GCATGATGCTCCATTGACACGTGACTTCTCGTCTCCTTTCTTAAATATATCTAAACAAACACTCCTACCTCTTCCAAAAATATATACACATC
 M A D T A R G T H H D
 34 TTTTGTGATCATCTCTCATTCAAATCTCATTCTCTCTAGTAAACAAGAACAAAAAATGGCGGATACAGCTAGAGGAAACCCATCAGAT
 I I G R D O Y P M H G R D R D O Y Q M S G R G S D Y S K S R
 124 ATCATGGCAGAGACCACTAGTACCGATGATGGGCGGAGACCGAGACCACTACAGATGCTCGGACGAGGATCTGCACTACTCCAAGCTTAGG
 O I A K A A T A V T A G G S L L V L S S L T L V G T V I A L
 214 CAGATTCTAAAGCTGCAACTGCTGTCACAGCTGGTGGTTCCCTCTCTGTTCTCTCCAGCCTTACCCTTGTGGAATGTCTATAGCTTTG
 T V A T P L L V I F S P I L V P A L I T V A L L I T G F L S
 214 ACTGTTGCAACACCTCTGCTGTTATCTTTCAGCCCAATCCTTGTCCCGGCTCTCATCACAGTTGCACTCCTCATCACCGGTTTCTTTCC
 S G G F G I A A A I T V F S W I Y K
 304 TCTGGAGGGTTTGGCATTGCCGCTATAACGTTTCTCTTGGATTACAAgtaagcacacatttatcatcttacttcataattttgtgca
 394 atatgtgcatgcatgtgttgagccagtagctttggatcaatttttttgggtcgataaacaatgtaacaataagaattgcaaatcttagg
 484 gaacatttgggttaactaaatacgaattttgacctagctagcttgaatgtgtctgtgtatatcatcttatataggttaaatgcttggtaga
 Y A T G E H P O G S D K L D S A R M K L G S K
 574 tacctattgattgtgaatagctACGCAACGGGAGAGCCCAAGGATCAGACAAAGTTGACAGCTGCAAGGATGAAGTTGGGAAGCAAA
 A O D L K D R A O Y Y G O Q H T G G E H D R D R T R G G O H
 664 GCTCAGGATCTGAAAGACAGAGCTCAGTACTACGGACAGCAACATACTGGTGGGGAACAAGACCGTGACCGTACTCGTGGTGGGCAACAC
 T T
 754 ACTACTTAAGTTACCCCACTGATGTCACTCGTCACTAGTCCAATAAATCCAATGTCCGGGAGTTAGTTTATGAGGAATAAAGTGTTTAGAAT
 KpnI
 844 TTGATCAGGGGGAGATAAATAAAGGCCGAGTTTGAATCTTTTGTGTTATAAGTAATGTTTATGCTGTGTTTCTATATGTTGTCAAATGCTAGC

FIGURE 3

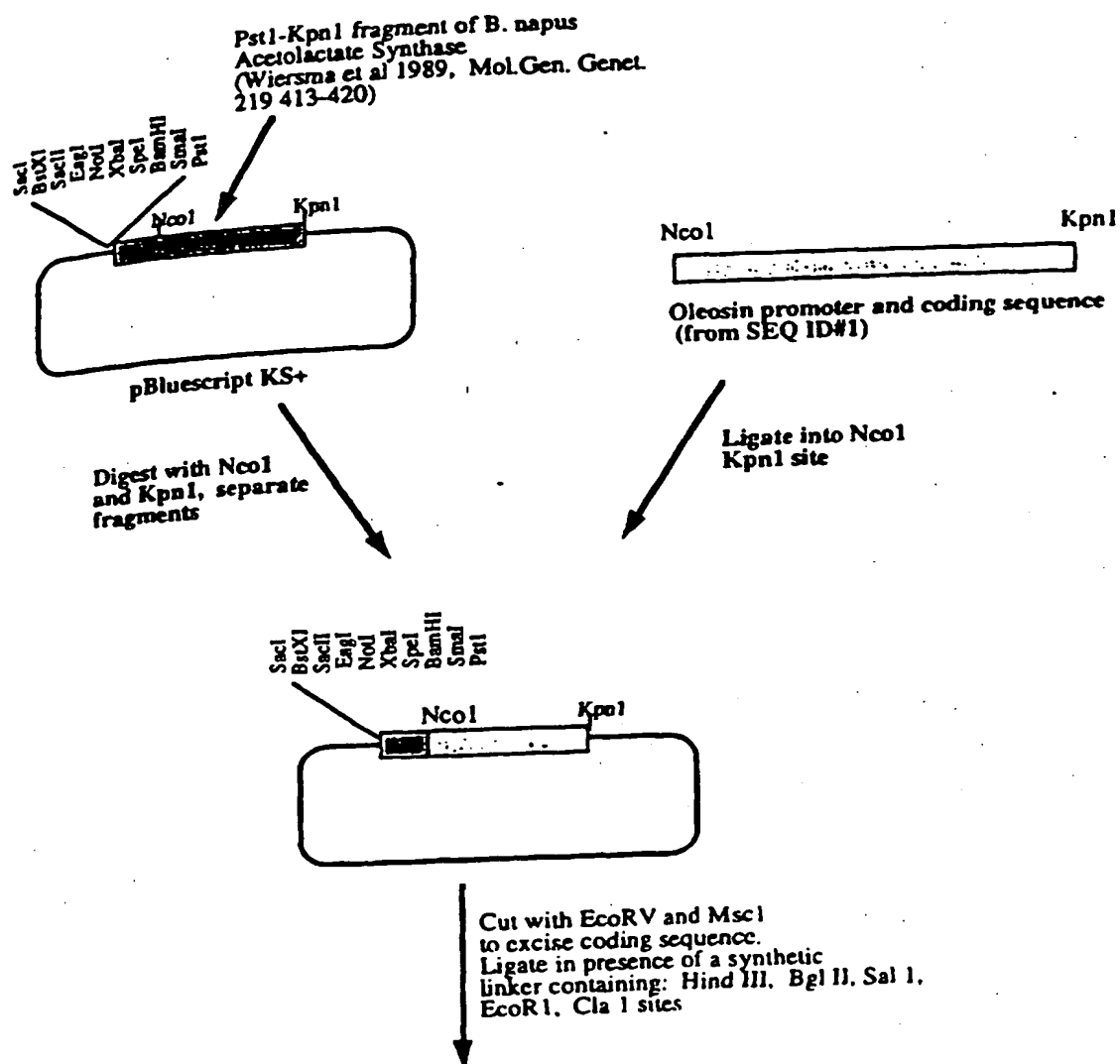


FIGURE 4

1	ATG GCG GAT ACA GCT AGA ACC CAT CAC GAT GTC ACA AGT CGA GAT CAG TAT CCC CGA GAC	60
1	N A D T A R T H B D V T S R D Q Y P R D	20
61	CGA GAC CAG TAT TCT ATG ATC GGT CGA GAC CGT GAC CAG TAC TCT ATG ATG GGC CGA GAC	120
21	R D Q Y S M I G R D R D Q Y S M M G R D	40
121	CGA GAC CAG TAC AAC ATG TAT GGT CGA GAC TAC TOC AAG TCT AGA CAG ATT GCT AAG GCT	180
41	R D Q Y N M Y G R D Y S K S R Q I A K A	60
181	GTT ACC GCA GTC ACG GCG GGT GGG TOC CTC CTT GTC CTC TOC AGT CTC ACC CTT GTT GGT	240
61	V T A V T A G G S L L V L S S L T L V G	80
241	ACT GTC ATT GCT TTG ACT GTT GCC ACT CCA CTC CTC GTT ATC TTT AGC CCA ATC CTC GTG	300
81	T V I A L T V A T P L L V I F S P I L V	100
301	CCG GCT CTC ATC ACC GTA GCA CTT CTC ATC ACT GGC TTT CTC TOC TCT GGT GGG TTT GCC	360
101	P A L I T V A L L I T G F L S S G G F A	120
361	ATT GCA GCT ATA ACC GTC TTC TOC TGG ATC TAT AAG TAC GCA ACG GGA GAG CAC CCA CAG	420
121	I A A I T V F S W I Y K Y A T G E H P Q	140
421	GGC TCA GAT AAG TTG GAC AGT GCA AGG ATG AAG CTG GGA ACC AAA GCT CAG GAT ATT AAA	480
141	C S D K L D S A R M K L G T K A Q D I K	160
481	GAC AGA GCT CAA TAC TAC GGA CAG CAA CAT ACA GGT GGT GAG CAT GAC CGT GAC CGT ACT	540
161	D R A Q Y Y G Q Q H T G G E H D R D R T	180
541	CGT GGT GGC CAG CAC ACT ACT TAA	564
181	R G G Q H T T *	188

FIGURE 5

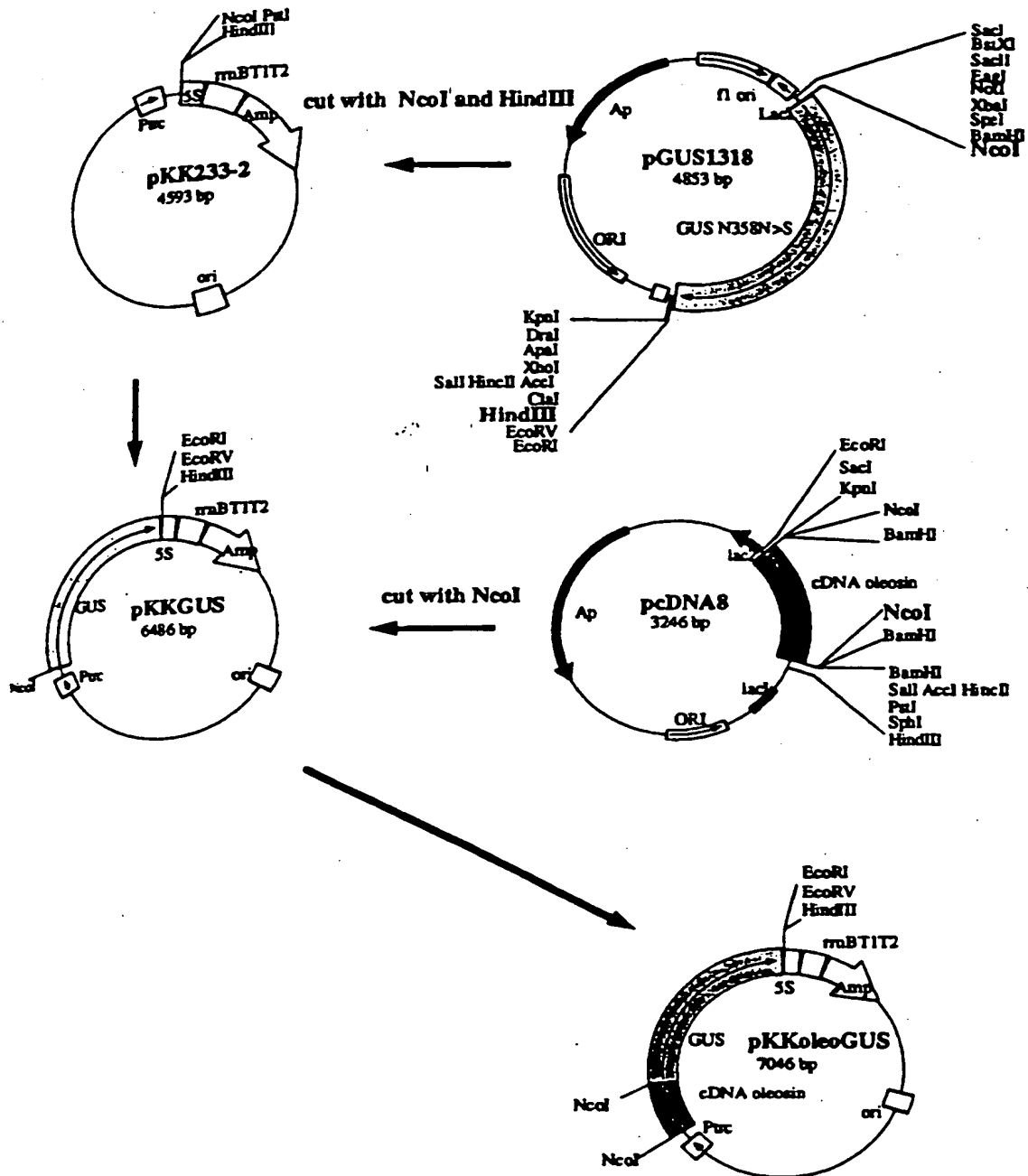


FIGURE 6

1	ATAAGCTTGCATGCCTGCCGAACTCTCTGGTAAGCTAGCTCCACTCCCCAGAAACAACCG	60
61	CGCCCAAATTGCCGGAATTGCTGACCTGAAGACGGAACATCATCGTCGGGTCTCTGGGCG	120
121	ATTGCCGGCGGAAGATGGGTACGCTTGGGCTTGAGGACGAGACCCGAATCGAGTCTGTGA	180
181	AAGGTTGTTTCATTGGGATTGTATACGGAGATTGGTCGTCGAGAGGTTTGAGGGAAAGGA	240
241	CAAATGGGTTTGGCTCTGGAGAAAGAGAGTGGGCTTTAGAGAGAGAATTGAGAGGTTTA	300
301	GAGAGAGATGCGGGCGGATGACGGGAGGAGAGACGACGAGGACCTGCATTATCAAAGCA	360
361	GTGACGTGGTGAAATTTGGAACCTTTAAGAGGCAGATAGATTTATTATTTGTATCCATT	420
421	TCTTCATTGTTCTAGAAATGTCGCGGAACAAATTTTAAACTAAATCCTAAATTTTCTAA	480
481	TTTTGTTGCCAATAGTGGATATGTGGGCCGTATAGAAGGAATCTATTGAAGGCCCAAACC	540
541	CATACTGACGAGCCCAAAGGTTTCGTTTTCGTTTATGTTTCGTTTCGATGCCAACGCCA	600
601	CATTCTGAGCTAGGCAAAAAACAAACGTGTCTTTGAATAGACTCCTCTCGTTAACACATG	660
661	CAGCGGCTGCATGGTGACGCCATTAAACAGTGGCCTACAATTGCATGATGTCTCCATTGA	720
721	CACGTGACTTCTCGTCTCCTTTCTTAATATATCTAACAAACACTCCTACCTCTTCAAAA	780
781	TATATACACATCTTTTGATCAATCTCTCATTCAAAATCTCATTCTCTCTAGTAAACAAG	840
	M A D T A R G T H H D I I G R D Q	
841	AACAAAAAATGGCGGATACAGCTAGAGGAACCCATCAGGATATCATCGGCAGAGACCAG	900
	Y P M H M G R D R D Q Y Q M S G R G S D Y	
901	TACCCGATGATGGGCCGAGACCGAGACCAGTACCAGATGTCCGGACGAGGATCTGACTAC	960
	S K S R Q I A K A A T A V T A G G S L L	
961	TCCAAGTCTAGGCAGATTGCTAAAGCTGCAACTGCTGTACAGCTGGTGGTTCCCTCCTT	1020
	V L S S L T L V G T V I A L T V A T P L	
1021	GTCTCTCCAGCCTTACCCTTGTGGAACCTGTATAGCTTTGACTGTTGCAACACCTCTG	1080
	L V I P S P I L V P A L I T V A L L I T	
1081	CTCGTTATCTTCAGCCCAATCCTTGTCCCGGCTCTCATCACAGTTGCACTCCTCATCACC	1140
	G F L S S G G F G I A A I T V F S W I Y	
1141	GGTTTTCTTTCCTCTGGAGGGTTTGGCATTGCCCTATAACCGTTTTCTCTTGGATTTC	1200
	K	
1201	AAGTAAGCACACATTTATCATCTTACTTTCATAATTTTGTGCAATATGTGCATGCATGTGT	1260
1261	TGAGCCAGTAGCTTTGGATCAATTTTTTGGTCAATAACAAATGTAAACAATAAGAAAT	1320
1321	GCAAAATCTAGGGAACATTTGGTTAACTAAATACGAAATTTGACCTAGCTAGCTTGAATG	1380
1381	TGTCTGTGTATATCATCTATATAGGTAAAAATGCTTGGTATGATACCTATTGATTGTGAAT	1440
	Y A T G E H P Q G S D K L D S A R M K	
1441	AGGTACGCAACGGGAGAGCACCCACAGGGATCAGACAAGTTGGACAGTGCAAGGATGAAG	1500
	L G S K A Q D L K D R A Q Y Y G Q Q H T	
1501	TTGGGAAGCAAAGCTCAGGATCTGAAAGACAGAGCTCAGTACTACGGACAGCAACATACT	1560
	G G E H D R D R T R G G Q H T T L V P R	
1561	GGTGGGGAACATGACCGTGACCGTACTCGTGGTGGCCAGCACACTACTCTCGTTCCACGA	1620
	G S M A E I T R I P L Y K G K S L R K A	
1621	GGATCCATGGCTGAGATCACCAGGATCCCTCTGTACAAAGGCAAGTCTCTGAGGAAGGCG	1680
	L K E H G L L E D F L Q K Q Q Y G I S S	
1681	CTGAAGGAGCATGGGCTTCTGGAGGACTTCTGCAGAAACAGCAGTATGGCATCAGCAGC	1740
	K Y S G F G E V A S V P L T N Y L D S Q	
1741	AAGTACTCCGGCTTCGGGGAGGTGCCAGCGTGCCCTGACCAACTACCTGGATAGTCAG	1800

FIGURE 6 cont'd

	Y F G K I Y L G T P P Q E F T V L F D T	
1801	TACTTTGGGAAGATCTACCTCGGGACCCCGCCCCAGGAGTTCACCGTGCTGTTTGACACT	1860
	G S S D F W V P S I Y C K S N A C K N H	
1861	GGCTCCTCTGACTTCTGGGTACCCTCTATCTACTGCAAGAGCAATGCCTGCAAAAACCAC	1920
	Q R P D P R K S S T F Q N L G K P L S I	
1921	CAGCGCTTCGACCCGAGAAAGTCGTCCACCTTCCAGAACCTGGGCAAGCCCCTGTCTATC	1980
	H Y G T G S M Q G I L G Y D T V T V S N	
1981	CACTACGGGACAGGCAGCATGCAGGGCATCCTGGGCTATGACACCGTCACTGTCTCCAAC	2040
	I V D I Q Q T V G L S T Q E P G D V F T	
2041	ATTGTGGACATCCAGCAGCAGTAGGCCTGAGCACCCAGGAGCCCGGGGACGTCTTCACC	2100
	Y A E F D G I L G M A Y P S L A S E Y S	
2101	TATGCCGAATTCGACGGGATCCTGGGGATGGCCTACCCCTCGCTCGCCTCAGAGTACTCG	2160
	I P V F D N M M N R H L V A Q D L F S V	
2161	ATACCCGTGTTTGACAACATGATGAACAGGCACCTGGTGGCCCAAGACCTGTTCTCGGTT	2220
	Y M D R N G Q E S M L T L G A I D P S Y	
2221	TACATGGACAGGAATGGCCAGGAGAGCATGCTCACGCTGGGGGCCATCGACCCGTCCTAC	2280
	Y T G S L H W V P V T V Q Q Y W Q F T V	
2281	TACACAGGGTCCCTGCACTGGGTGCCCCGTGACAGTGCAGCAGTACTGGCAGTTCACTGTG	2340
	D S V T I S G V V V A C E G G C Q A I L	
2341	GACAGTGTACCATCAGCGGTGTGGTTGTGGCCTGTGAGGGTGGCTGTGAGGCCATCTTG	2400
	D T G T S K L V G P S S S D I L N I Q Q A	
2401	GACACGGGCACCTCCAAGCTGGTGGGGCCAGCAGCGACATCCTCAACATCCAGCAGGCC	2460
	I G A T Q N Q Y G E F D I D C D N L S Y	
2461	ATTGGAGCCACACAGAACCAGTACGGTGAGTTTGACATCGACTGCGACAACCTGAGCTAC	2520
	N P T V V F E I N G K M Y P L T P S A Y	
2521	ATGCCCCACTGTGGTCTTTGAGATCAATGGCAAAATGTACCCACTGACCCCTCCGCCTAT	2580
	T S Q D Q G F C T S G F Q S E N H S Q K	
2581	ACCAGCCAAGACCAGGGCTTCTGTACCAGTGGCTTCCAGAGTGAAAATCATTCCCAGAAA	2640
	W I L G D V F I R E Y Y S V F D R A N N	
2641	TGGATCCTGGGGGATGTTTTCATCCGAGAGTATTACAGCGTCTTTGACAGGGCCAACAAC	2700
	L V G L A K A I *	
2701	CTCGTGGGGCTGGCCAAAGCCATCTGAAAGCTT	2733

HindIII

FIGURE 7

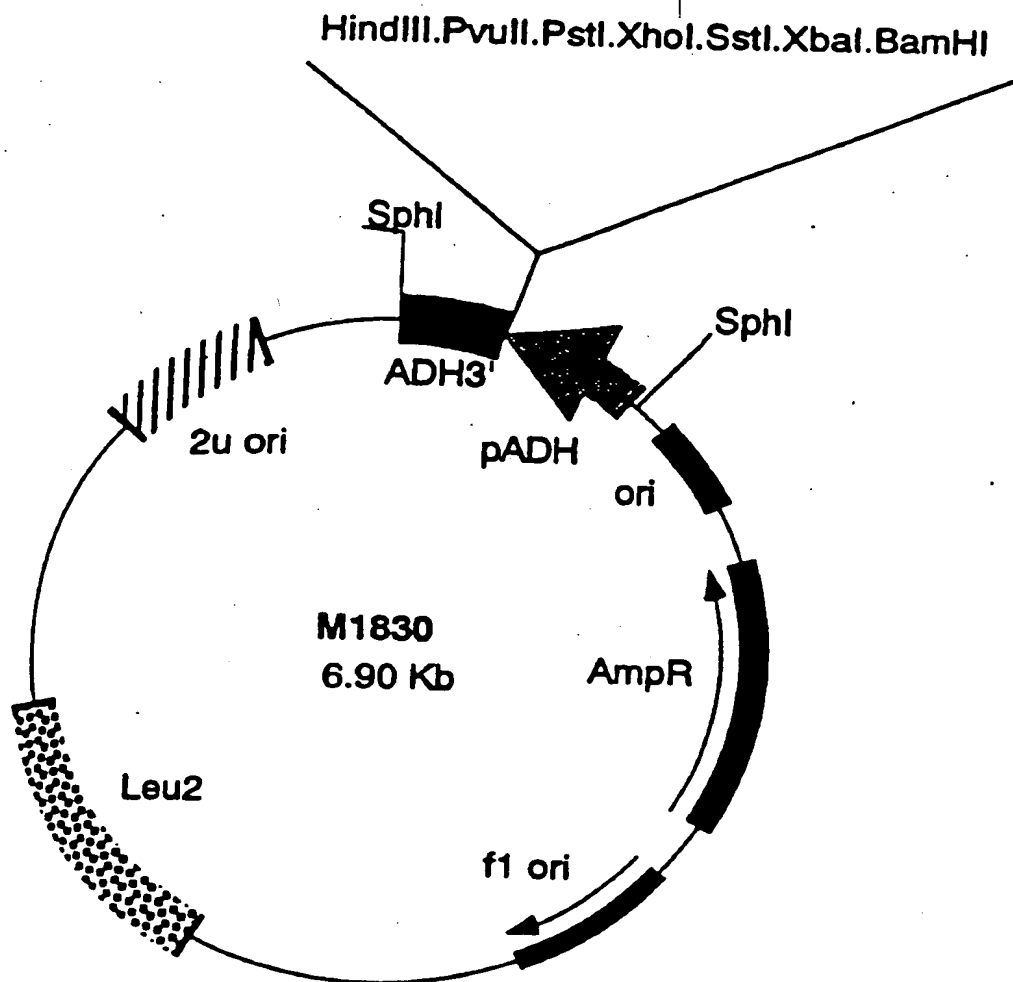


FIGURE 8

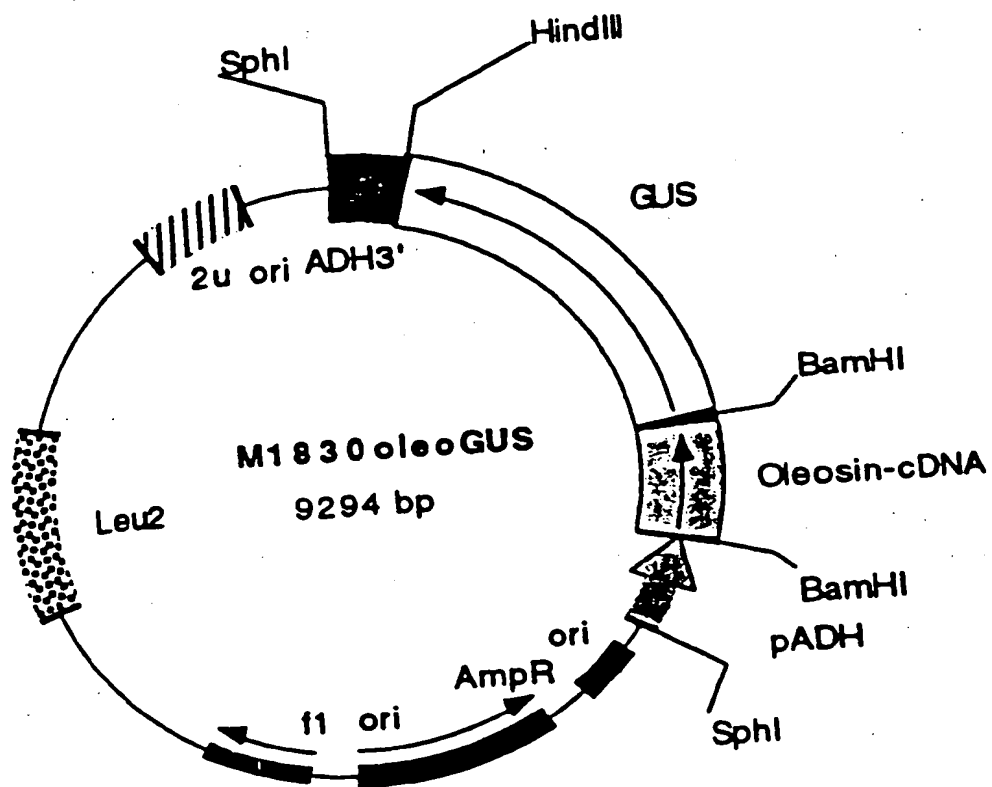


FIGURE 9

Sequence alignment of the isolated caleosin (this application) with the coding sequence of the reported caleosin gene (accession number AF067857). Indicated are the primers GVR979 and GVR980 used for the polymerase Chain Reaction and the one nucleotide change (position 69).

ClustalW Formatted Alignments

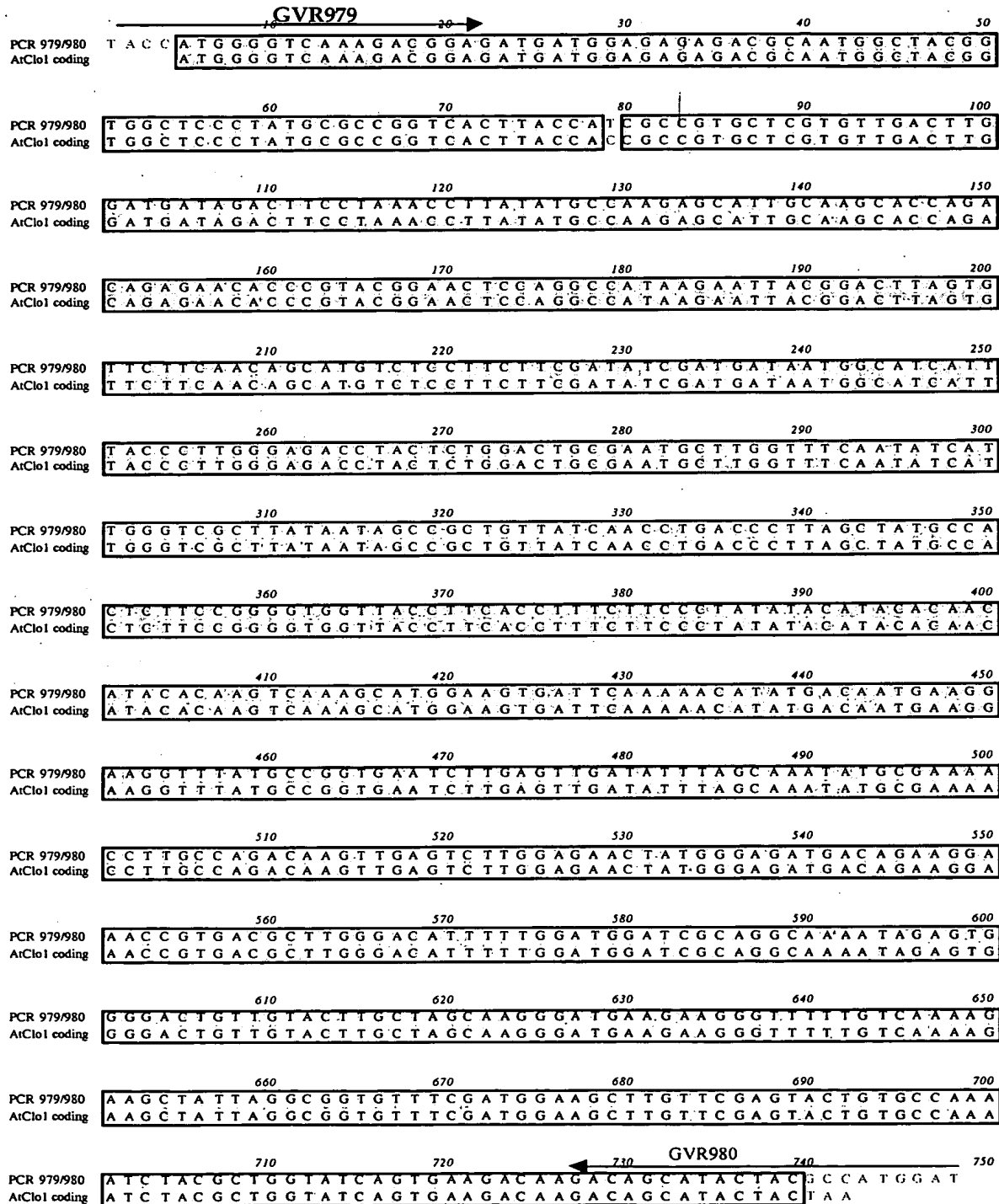


FIGURE 10

Nucleotide sequence of insert of pSBS2098 containing the phaseolin promoter-B Glucuronidase (GUS)-phaseolin terminator sequence. The GUS sequence and its deduced amino acid sequence is indicated in uppercase. The phaseolin promoter corresponds to nucleotide 1-1547, and the phaseolin terminator corresponds to nucleotide sequence 3426-4646. The terminator was furnished with a KpnI site (nt 4647-4652) to facilitate cloning.

EcoRI																					
1	gaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggttttttacctctattttaagggg																			80	
81	ttttccacctaaaaattctggtatcattctcactttacttgttactttaattttctcataatctttggttgaaattatcac																			160	
161	gcttccgcacacgatatccctacaaattttatttttgttaaaccattttcaaaccgcataaaattttatgaagtcctcgtct																			240	
241	atctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggttagaaagcataaagattt																			320	
321	attcttattcttcttcatataaatgtttaatatacaataaaacaaattctttacctaagaaggatttcccattttata																			400	
401	ttttaaaaatatatttatcaaatattttcaaccacgtaaatctcataataataagtgtgttccaaaagtaataaaattta																			480	
481	actccataatttttttatttcgactgatcttaagcaacacccagtgacacaactagccatttttttctttgaaataaaaa																			560	
561	atccaattatcattgtattttttttatacaatgaaaatttcaccaaaacaatcatttgtgggtatttctgaagcaagtc																			640	
641	ttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacatcttcta																			720	
721	aagtaatttttaataatagttactatattcaagatttcataatatcaaatactcaatattacttctaaaaaattaattagat																			800	
801	ataattaaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgattttatttctactactgtttaa																			880	
881	attgtttttatagattgtttaagtaataagtaattgtagagattgttagagtggtaccctaaaccataaacataaac																			960	
961	atttatggtggactaaattttcatataattcttattgtcttttactctttcttggtagtgaagtcgtaactagaattacag																			1040	
1041	tgggttgccatgacactctgtgggtcttttgggttcabgcatgggtctctgcgcaagaaaaagacaaagaacaaagaaaaaag																			1120	
1121	acaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactgggtgatcaagatcgccgctccatgtat																			1200	
1201	gtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatgggtcacccatctcaaccacacacaaacacat																			1280	
1281	tgcttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttctacttcaacaca																			1360	
1361	cgtcaacctgcataatgcgtgtcatcccatgccc aaatctccatgcatgttccaaccaccttctctcttatataataccta																			1440	
1441	taaatacctctaataatcactcacttctttcatcatccatccatccagagtactactactctactactataataacccaac																			1520	
1521	ccaactcatattcaatactactctaCC ATG GTC TTA CGT CCT GTA GAA ACC CCA ACC CGT GAA ATC																			1586	
1	M V L R P V E T P T R E I																			13	
1587	AAA	AAA	CTC	GAC	GGC	CTG	TGG	GCA	TTC	AGT	CTG	GAT	CGC	GAA	AAC	TGT	GGA	ATT	GAT	CAG	1646
14	K	K	L	D	G	L	W	A	F	S	L	D	R	E	N	C	G	I	D	Q	33
1647	CGT	TGG	TGG	GAA	AGC	GCG	TTA	CAA	GAA	AGC	CGG	GCA	ATT	GCT	GTG	CCA	GGC	AGT	TTT	AAC	1706
34	R	W	W	E	S	A	L	Q	E	S	R	A	I	A	V	P	G	S	F	N	53
1707	GAT	CAG	TTC	GCC	GAT	GCA	GAT	ATT	CGT	AAT	TAT	GCG	GGC	AAC	GTC	TGG	TAT	CAG	CGC	GAA	1766
54	D	Q	F	A	D	A	D	I	R	N	Y	A	G	N	V	W	Y	Q	R	E	73
1767	GTC	TTT	ATA	CCG	AAA	GGT	TGG	GCA	GGC	CAG	CGT	ATC	GTG	CTG	CGT	TTC	GAT	GCG	GTC	ACT	1826
74	V	F	I	P	K	G	W	A	G	Q	R	I	V	L	R	F	D	A	V	T	93
1827	CAT	TAC	GGC	AAA	GTG	TGG	GTC	AAT	AAT	CAG	GAA	GTG	ATG	GAG	CAT	CAG	GGC	GGC	TAT	ACG	1886
94	H	Y	G	K	V	W	V	N	N	Q	E	V	M	E	H	Q	G	G	Y	T	113
1887	CCA	TTT	GAA	GCC	GAT	GTC	ACG	CCG	TAT	GTT	ATT	GCC	GGG	AAA	AGT	GTA	CGT	ATC	ACC	GTT	1946
114	P	F	E	A	D	V	T	P	Y	V	I	A	G	K	S	V	R	I	T	V	133
1947	TGT	GTG	AAC	AAC	GAA	CTG	AAC	TGG	CAG	ACT	ATC	CCG	CCG	GGA	ATG	GTG	ATT	ACC	GAC	GAA	2006
134	C	V	N	N	E	L	N	W	Q	T	I	P	P	G	M	V	I	T	D	E	153
2007	AAC	GGC	AAG	AAA	AAG	CAG	TCT	TAC	TTC	CAT	GAT	TTC	TTT	AAC	TAT	GCC	GGA	ATC	CAT	CGC	2066
154	N	G	K	K	K	Q	S	Y	F	H	D	F	F	N	Y	A	G	I	H	R	173
2067	AGC	GTA	ATG	CTC	TAC	ACC	ACG	CCG	AAC	ACC	TGG	GTG	GAC	GAT	ATC	ACC	GTG	GTG	ACG	CAT	2126
174	S	V	M	L	Y	T	T	P	N	T	W	V	D	D	I	T	V	V	T	H	193
2127	GTC	GCG	CAA	GAC	TGT	AAC	CAC	GCG	TCT	GTT	GAC	TGG	CAG	GTG	GTG	GCC	AAT	GGT	GAT	GTC	2186
194	V	A	Q	D	C	N	H	A	S	V	D	W	Q	V	V	A	N	G	D	V	213
2187	AGC	GTT	GAA																		

FIGURE 10 (cont'd)

2247	ACT	TTG	CAA	GTG	GTG	AAT	CCG	CAC	CTC	TGG	CAA	CCG	GGT	GAA	GGT	TAT	CTC	TAT	GAA	CTG	2306
234	T	L	Q	V	V	N	P	H	L	W	Q	P	G	E	G	Y	L	Y	E	L	253
2307	TGC	GTC	ACA	GCC	AAA	AGC	CAG	ACA	GAG	TGT	GAT	ATC	TAC	CCG	CTT	CGC	GTC	GGC	ATC	CGG	2366
254	C	V	T	A	K	S	Q	T	E	C	D	I	Y	P	L	R	V	G	I	R	273
2367	TCA	GTG	GCA	GTG	AAG	GGC	CAA	CAG	TTC	CTG	ATT	AAC	CAC	AAA	CCG	TTC	TAC	TTT	ACT	GGC	2426
274	S	V	A	V	K	G	Q	Q	F	L	I	N	H	K	P	F	Y	F	T	G	293
2427	TTT	GGT	CGT	CAT	GAA	GAT	GCG	GAC	TTA	CGT	GGC	AAA	GGA	TTC	GAT	AAC	GTG	CTG	ATG	GTG	2486
294	F	G	R	H	E	D	A	D	L	R	G	K	G	F	D	N	V	L	M	V	313
2487	CAC	GAC	CAC	GCA	TTA	ATG	GAC	TGG	ATT	GGG	GCC	AAC	TCC	TAC	CGT	ACC	TCG	CAT	TAC	CCT	2546
314	H	D	H	A	L	M	D	W	I	G	A	N	S	Y	R	T	S	H	Y	P	333
2547	TAC	GCT	GAA	GAG	ATG	CTC	GAC	TGG	GCA	GAT	GAA	CAT	GGC	ATC	GTG	GTG	ATT	GAT	GAA	ACT	2606
334	Y	A	E	E	M	L	D	W	A	D	E	H	G	I	V	V	I	D	E	T	353
2607	GCT	GCT	GTC	GGC	TTT	TCG	CTC	TCT	TTA	GGC	ATT	GGT	TTC	GAA	GCG	GGC	AAC	AAG	CCG	AAA	2666
354	A	A	V	G	F	S	L	S	L	G	I	G	F	E	A	G	N	K	P	K	373
2667	GAA	CTG	TAC	AGC	GAA	GAG	GCA	GTC	AAC	GGG	GAA	ACT	CAG	CAA	GCG	CAC	TTA	CAG	GCG	ATT	2726
374	E	L	Y	S	E	E	A	V	N	G	E	T	Q	Q	A	H	L	Q	A	I	393
2727	AAA	GAG	CTG	ATA	GCG	CGT	GAC	AAA	AAC	CAC	CCA	AGC	GTG	GTG	ATG	TGG	AGT	ATT	GCC	AAC	2786
394	K	E	L	I	A	R	D	K	N	H	P	S	V	V	M	W	S	I	A	N	413
2787	GAA	CCG	GAT	ACC	CGT	CCG	CAA	GGT	GCA	CGG	GAA	TAT	TTC	GCG	CCA	CTG	GCG	GAA	GCA	ACG	2846
414	E	P	D	T	R	P	Q	G	A	R	E	Y	F	A	P	L	A	E	A	T	433
2847	CGT	AAA	CTC	GAC	CCG	ACG	CGT	CCG	ATC	ACC	TGC	GTC	AAT	GTA	ATG	TTC	TGC	GAC	GCT	CAC	2906
434	R	K	L	D	P	T	R	P	I	T	C	V	N	V	M	F	C	D	A	H	453
2907	ACC	GAT	ACC	ATC	AGC	GAT	CTC	TTT	GAT	GTG	CTG	TGC	CTG	AAC	CGT	TAT	TAC	GGA	TGG	TAT	2966
454	T	D	T	I	S	D	L	F	D	V	L	C	L	N	R	Y	Y	G	W	Y	473
2967	GTC	CAA	AGC	GGC	GAT	TTG	GAA	ACG	GCA	GAG	AAG	GTA	CTG	GAA	AAA	GAA	CTT	CTG	GCC	TGG	3026
474	V	Q	S	G	D	L	E	T	A	E	K	V	L	E	K	E	L	L	A	W	493
3027	CAG	GAG	AAA	CTG	CAT	CAG	CCG	ATT	ATC	ATC	ACC	GAA	TAC	GGC	GTG	GAT	ACG	TTA	GCC	GGG	3086
494	Q	E	K	L	H	Q	P	I	I	I	T	E	Y	G	V	D	T	L	A	G	513
3087	CTG	CAC	TCA	ATG	TAC	ACC	GAC	ATG	TGG	AGT	GAA	GAG	TAT	CAG	TGT	GCA	TGG	CTG	GAT	ATG	3146
514	L	H	S	M	Y	T	D	M	W	S	E	E	Y	Q	C	A	W	L	D	M	533
3147	TAT	CAC	CGC	GTC	TTT	GAT	CGC	GTC	AGC	GCC	GTC	GTC	GGT	GAA	CAG	GTA	TGG	AAT	TTC	GCC	3206
534	Y	H	R	V	F	D	R	V	S	A	V	V	G	E	Q	V	W	N	F	A	553
3207	GAT	TTT	GCG	ACC	TCG	CAA	GGC	ATA	TTG	CGC	GTT	GGC	GGT	AAC	AAG	AAA	GGG	ATC	TTC	ACT	3266
554	D	F	A	T	S	Q	G	I	L	R	V	G	G	N	K	K	G	I	F	T	573
3267	CGC	GAC	CGC	AAA	CCG	AAG	TCG	GCG	GCT	TTT	CTG	CTG	CAA	AAA	CGC	TGG	ACT	GGC	ATG	AAC	3326
574	R	D	R	K	P	K	S	A	A	F	L	L	Q	K	R	W	T	G	M	N	593
3327	TTC	GGT	GAA	AAA	CCG	CAG	CAG	GGA	GGC	AAA	CAA	TGA	ATCAACA	ACTCTCCTGGCGC	ACCATCGTCGGC						3394
594	F	G	E	K	P	Q	Q	G	G	K	Q	*									605
3395	TACAGCCTCGGTGGAATTCGATATCAAGCTTaaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagc	3474																			
3475	atggaatatgtatccgaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaaggatgtt	3554																			
3555	atgatataattaacactctatctatgcaccttattgttctatgataaaatctcttattattataaaatcatctgaatcgt	3634																			
3635	gacggcttatggaatgcttcaaatagtacaaaaacaaatgtgtactataagacttttctaacaattctaacttttagcatt	3714																			
3715	gtgaacgagacataagtgttaagaagacataacaattataatggaagaagtttgtctccatttatatattatattatattacc	3794																			
3795	cacttatgtattatatttaggatgttaaggagacataacaattataaagagagaagtttgtatccatttatatattatata	3874																			
3875	ctaccatttatattatattatacttatacttattttaatgtctttataaggtttgatccatgatatttctaataatttttagt	3954																			
3955	tgatatgtatatgaaaggttactatttgaactctcttactctgtataaaggttgatcatccttaaagtggttctattta	4034																			
4035	attttattgtcttcttacagataaaaaaaaaattatgagttggtttgataaaaatttgaaggatttaaaataataataaat	4114																			
4115	aataaataacatataatataatgtatatataaatttattataatataacatttatctataaaaaagtaaatattgtcataaat	4194																			

FIGURE 10 (cont'd)

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4195 ctatacaatcgtttagccttgctggacgactctcaattatTTTaaacgagagtaaacaTatttgactTTTTtggttatttaa 4274
4275 caaattattatttaacactatatgaaatTTTTTTTTTTTatcggcaaggaaataaaattaaattaggagggacaatggTg 4354
4355 tgtcccaatccttatacaaccaacttccacaggaaggTcaggtcggggacaacaaaaaacaggcaagggaattTTTTta 4434
4435 atttgggttgTcttgTTtgctgcataatttatgcagTaaaacactacacataaccctTTtagcagtagagcaatggTtga 4514
4515 ccgtgtgcttagcttctTTTattTTTattTTTTTatcagcaagaataaaataaaataaaatgagacacttcagggatgTtt 4594
4595 caacccttatacaaaacccccaaaaacaagtttccttagcaccctaccaactaaGGTACC 4652
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FIGURE 11

Nucleotide sequence of the phaseolin promoter-oleosinGUS-phaseolin terminator sequence. The oleosinGUS coding sequence and its deduced amino acid sequence is indicated. The phaseolin promoter corresponds to nucleotide 6-1554. The sequence encoding oleosin corresponds to nt 1555-2313, the intron in this sequence (nt 1908-2147) is indicated in italics. The GUS sequence corresponds to nt 2314-4191. The phaseolin terminator corresponds to nucleotide sequence 4192-5412.

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PstI   EcoRI
1  ctgcaggaattcattgtactcccagtatcattatagtgaaagtttggctctctcgccggtggttttttacctctattta 80
81  aaggggttttccacctaaaaattctggtatcattctcactttacttggtactttaattctcataatctttggttgaat 160
161  tatcacgcttccgcacacgatatccctacaaaatttattttgttaaaccattttcaaaccgcataaaattttatgaagtc 240
241  cegtctatctttaaagttagtctaaccattttcatattgaaatatataatttacttaatttttagcgttggtagaagcataa 320
321  tgatttattcttattcttcttcatataaatgtttaatatatacaatataaacaattctttaccttaagaaggatttcccat 400
401  tttatattttaaaaatatatttatacaaattttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480
481  aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccattttttcttttgat 560
561  aaaaaaatccaattatcattgtatttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaa 640
641  gtcattgttatgcaaaattctataatttccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720
721  cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800
801  ttagatataaataaataattacttttttaattttaagtttaattgttggaatttgtgactattgatttatttctactat 880
881  gtttaaattgttttatagatagtttaaagtaaatataagtaagttagtagagtggttagagtggtaccctaaccataaac 960
961  tataagattttatggtggactaattttcatatatttcttattgcttttacctttcttggtagtaagtcogtaactggaa 1040
1041  ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120
1121  aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200
1201  catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcaccctctcaaccacacacaca 1280
1281  aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttctactt 1360
1361  caacacacgtcaacctgcataatgcgtgtcatccccatgcccaatctccatgcatttccaaccaccttctctcttatata 1440
1441  atacctataaataacctctaatactactctactcttcttctcatcatccatccatccagagtactactactctactactataata 1520
1521  ccccaacccaactcatattcaatactactctact ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT 1587
1      M A D T A R G T H H D 11
1588 ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC 1647
12 I I G R D Q Y P M M G R D R D Q Y Q M S 31
1648 GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA 1707
32 G R G S D Y S K S R Q I A K A A T A V T 51
1708 GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG 1767
52 A G G S L L V L S S L T L V G T V I A L 71
1768 ACT GTT GCA ACA CCT CTG CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA 1827
72 T V A T P L L V I F S P I L V P A L I T 91
1828 GTT GCA CTC CTC ATC ACC GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC 1887
92 V A L L I T G A F L S S G G F G I A A I T 111
1888 GTT TTC TCT TGG ATT TAC AA gtaagcacacatttatcatcttacttcataattttgtgcaatatgtgcatgca 1960
112 V F S W I Y K 118
1961 tgtgttgagccagtagctttggatcaatttttttggtcgaataacaaatgtaacaataagaaattgcaaattctagggaa 2040
2041 catttgggttaactaaatacgaattttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgctt 2120
2121 ggtagatgatactattgattgtgaatag G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG 2184
119 Y A T G E H P Q G S D K 130

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FIGURE 11 (cont'd)

2185	TTG	GAC	AGT	GCA	AGG	ATG	AAG	TTG	GGA	AGC	AAA	GCT	CAG	GAT	CTG	AAA	GAC	AGA	GCT	CAG	2244
131	L	D	S	A	R	M	K	L	G	S	K	A	Q	D	L	K	D	R	A	Q	150
2245	TAC	TAC	GGA	CAG	CAA	CAT	ACT	GGT	GGG	GAA	CAT	GAC	CGT	GAC	CGT	ACT	CGT	GGT	GGC	CAG	2304
151	Y	Y	G	Q	Q	H	T	G	G	E	H	D	R	D	R	T	R	G	G	Q	170
2305	CAC	ACT	ACC	ATG	GTC	TTA	CGT	CCT	GTA	GAA	ACC	CCA	ACC	CGT	GAA	ATC	AAA	AAA	CTC	GAC	2364
171	H	T	T	M	V	L	R	P	V	E	T	P	T	R	E	I	K	K	L	D	190
2365	GGC	CTG	TGG	GCA	TTC	AGT	CTG	GAT	CGC	GAA	AAC	TGT	GGA	ATT	GAT	CAG	CGT	TGG	TGG	GAA	2424
191	G	L	W	A	F	S	L	D	R	E	N	C	G	I	D	Q	R	W	W	E	210
2425	AGC	GCG	TTA	CAA	GAA	AGC	CGG	GCA	ATT	GCT	GTG	CCA	GGC	AGT	TTT	AAC	GAT	CAG	TTC	GCC	2484
211	S	A	L	Q	E	S	R	A	I	A	V	P	G	S	F	N	D	Q	F	A	230
2485	GAT	GCA	GAT	ATT	CGT	AAT	TAT	GCG	GGC	AAC	GTC	TGG	TAT	CAG	CGC	GAA	GTC	TTT	ATA	CCG	2544
231	D	A	D	I	R	N	Y	A	G	N	V	W	Y	Q	R	E	V	F	I	P	250
2545	AAA	GGT	TGG	GCA	GGC	CAG	CGT	ATC	GTG	CTG	CGT	TTC	GAT	GCG	GTC	ACT	CAT	TAC	GGC	AAA	2604
251	K	G	W	A	G	Q	R	I	V	L	R	F	D	A	V	T	H	Y	G	K	270
2605	GTG	TGG	GTC	AAT	AAT	CAG	GAA	GTG	ATG	GAG	CAT	CAG	GGC	GGC	TAT	ACG	CCA	TTT	GAA	GCC	2664
271	V	W	V	N	N	Q	E	V	M	E	H	Q	G	G	Y	T	P	F	E	A	290
2665	GAT	GTC	ACG	CCG	TAT	GTT	ATT	GCC	GGG	AAA	AGT	GTA	CGT	ATC	ACC	GTT	TGT	GTG	AAC	AAC	2724
291	D	V	T	P	Y	V	I	A	G	K	S	V	R	I	T	V	C	V	N	N	310
2725	GAA	CTG	AAC	TGG	CAG	ACT	ATC	CCG	CCG	GGA	ATG	GTG	ATT	ACC	GAC	GAA	AAC	GGC	AAG	AAA	2784
311	E	L	N	W	Q	T	I	P	P	G	M	V	I	T	D	E	N	G	K	K	330
2785	AAG	CAG	TCT	TAC	TTC	CAT	GAT	TTC	TTT	AAC	TAT	GCC	GGA	ATC	CAT	CGC	AGC	GTA	ATG	CTC	2844
331	K	Q	S	Y	F	H	D	F	F	N	Y	A	G	I	H	R	S	V	M	L	350
2845	TAC	ACC	ACG	CCG	AAC	ACC	TGG	GTG	GAC	GAT	ATC	ACC	GTG	GTG	ACG	CAT	GTC	GCG	CAA	GAC	2904
351	Y	T	T	P	N	T	W	V	D	D	I	T	V	V	T	H	V	A	Q	D	370
2905	TGT	AAC	CAC	GCG	TCT	GTT	GAC	TGG	CAG	GTG	GTG	GCC	AAT	GGT	GAT	GTC	AGC	GTT	GAA	CTG	2964
371	C	N	H	A	S	V	D	W	Q	V	V	A	N	G	D	V	S	V	E	L	390
2965	CGT	GAT	GCG	GAT	CAA	CAG	GTG	GTT	GCA	ACT	GGA	CAA	GGC	ACT	AGC	GGG	ACT	TTG	CAA	GTG	3024
391	R	D	A	D	Q	Q	V	V	A	T	G	Q	G	T	S	G	T	L	Q	V	410
3025	GTG	AAT	CCG	CAC	CTC	TGG	CAA	CCG	GGT	GAA	GGT	TAT	CTC	TAT	GAA	CTG	TGC	GTC	ACA	GCC	3084
411	V	N	P	H	L	W	Q	P	G	E	G	Y	L	Y	E	L	C	V	T	A	430
3085	AAA	AGC	CAG	ACA	GAG	TGT	GAT	ATC	TAC	CCG	CTT	CGC	GTC	GGC	ATC	CGG	TCA	GTG	GCA	GTG	3144
431	K	S	Q	T	E	C	D	I	Y	P	L	R	V	G	I	R	S	V	A	V	450
3145	AAG	GGC	CAA	CAG	TTC	CTG	ATT	AAC	CAC	AAA	CCG	TTC	TAC	TTT	ACT	GGC	TTT	GGT	CGT	CAT	3204
451	K	G	Q	Q	F	L	I	N	H	K	P	F	Y	F	T	G	F	G	R	H	470
3205	GAA	GAT	GCG	GAC	TTA	CGT	GGC	AAA	GGA	TTC	GAT	AAC	GTG	CTG	ATG	GTG	CAC	GAC	CAC	GCA	3264
471	E	D	A	D	L	R	G	K	G	F	D	N	V	L	M	V	H	D	H	A	490
3265	TTA	ATG	GAC	TGG	ATT	GGG	GCC	AAC	TCC	TAC	CGT	ACC	TCG	CAT	TAC	CCT	TAC	GCT	GAA	GAG	3324
491	L	M	D	W	I	G	A	N	S	Y	R	T	S	H	Y	P	Y	A	E	E	510
3325	ATG	CTC	GAC	TGG	GCA	GAT	GAA	CAT	GGC	ATC	GTG	GTG	ATT	GAT	GAA	ACT	GCT	GCT	GTC	GGC	3384
511	M	L	D	W	A	D	E	H	G	I	V	V	I	D	E	T	A	A	V	G	530
3385	TTT	TCG	CTC	TCT	TTA	GGC	ATT	GGT	TTC	GAA	GCG	GGC	AAC	AAG	CCG	AAA	GAA	CTG	TAC	AGC	3444
531	F	S	L	S	L	G	I	G	F	E	A	G	N	K	P	K	E	L	Y	S	550
3445	GAA	GAG	GCA	GTC	AAC	GGG	GAA	ACT	CAG	CAA	GCG	CAC	TTA	CAG	GCG	ATT	AAA	GAG	CTG	ATA	3504
551	E	E	A	V	N	G	E	T	Q	Q	A	H	L	Q	A	I	K	E	L	I	570
3505	GCG	CGT	GAC	AAA	AAC	CAC	CCA	AGC	GTG	GTG	ATG	TGG	AGT	ATT	GCC	AAC	GAA	CCG	GAT	ACC	3564
571	A	R	D	K	N	H	P	S	V	V	M	W	S	I	A	N	E	P	D	T	590

FIGURE 11 (cont'd)

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3565 CGT CCG CAA GGT GCA CGG GAA TAT TTC GCG CCA CTG GCG GAA GCA ACG CGT AAA CTC GAC 3624
591 R P Q G A R E Y F A P L A E A T R K L D 610
3625 CCG ACG CGT CCG ATC ACC TGC GTC AAT GTA ATG TTC TGC GAC GCT CAC ACC GAT ACC ATC 3684
611 P T R P I T C V N V M F C D A H T D T I 630
3685 AGC GAT CTC TTT GAT GTG CTG TGC CTG AAC CGT TAT TAC GGA TGG TAT GTC CAA AGC GGC 3744
631 S D L F D V L C L N R Y Y G W Y V Q S G 650
3745 GAT TTG GAA ACG GCA GAG AAG GTA CTG GAA AAA GAA CTT CTG GCC TGG CAG GAG AAA CTG 3804
651 D L E T A E K V L E K E L L A W Q E K L 670
3805 CAT CAG CCG ATT ATC ATC ACC GAA TAC GGC GTG GAT ACG TTA GCC GGG CTG CAC TCA ATG 3864
671 H Q P I I I T E Y G V D T L A G L H S M 690
3865 TAC ACC GAC ATG TGG AGT GAA GAG TAT CAG TGT GCA TGG CTG GAT ATG TAT CAC CGC GTC 3924
691 Y T D M W S E E Y Q C A W L D M Y H R V 710
3925 TTT GAT CGC GTC AGC GCC GTC GTC GGT GAA CAG GTA TGG AAT TTC GCC GAT TTT GCG ACC 3984
711 F D R V S A V V G E Q V W N F A D F A T 730
3985 TCG CAA GGC ATA TTG CGC GTT GGC GGT AAC AAG AAA GGG ATC TTC ACT CGC GAC CGC AAA 4044
731 S Q G I L R V G G N K K G I F T R D R K 750
4045 CCG AAG TCG GCG GCT TTT CTG CTG CAA AAA CGC TGG ACT GGC ATG AAC TTC GGT GAA AAA 4104
751 P K S A A F L L Q K R W T G M N F G E K 770
4105 CCG CAG CAG GGA GGC AAA CAA TGA ATCAACAACCTCTCCTGGCGCACCATCGTCGGCTACAGCCTCGGTGGAA 4176
771 P Q Q G G K Q * 778
4177 TTCGATATCAAGCTTaaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatcc 4256
4257 gaccatgtaacagtataataaactgagctccatctcacttcttctatgaataaacaaggatggttatgatatattaacact 4336
4337 ctatctatgcaccttattgttctatgataaatttctcttattattataaatcatctgaatcgtgacggcttatggaatg 4416
4417 cttcaaatagtacaaaaaacaatgtgtactataagactttctaaacaatttctaacttttagcattgtgaacgagacataag 4496
4497 tgtaagaagacataacaattataatggaagaagtttgtctccatttatatattatataattaccacttatgtattatat 4576
4577 taggatgtaaggagacataacaattataaagagagaagtttgtatccatttatatattatataactaccatttatatat 4656
4657 tatacttatccacttatttaattgtctttataagggtttgatccatgatattttctaataatttttagttgatatgtatatgaaa 4736
4737 gggactatttgaactctcttactctgtataaagggttgatcatccttaaagtggtctatttaattttattgcttctta 4816
4817 cagataaaaaaaaaattatgagttggtttgataaaatattgaaggatttaaaataataataaataaataaataacatataa 4896
4897 tatatgtatataaattttattataatataacatttatctataaaaaagtaaataattgtcataaatctatacaatcgtttag 4976
4977 ccttgctggacgactctcaattatttaaacgagagtaaacatatttgacttttttggttatttaacaaattattatttaac 5056
5057 actatatgaaattttttttttttatcgggcaaggaaataaaattaaattaggagggacaatgggtgtgtcccaatccttata 5136
5137 caaccaacttccacaggaaggtcaggtcggggacaacaaaaaacaggcaagggaatttttaatttgggtgtgtcttgt 5216
5217 ttgctgcataatttatgcagtaaaacactacataacccttttagcagtagagcaatgggttgaccgtgtgcttagcttc 5296
5297 ttttattttatttttttatcagcaagaataaaataaaataaaatgagacacttcagggatgtttcaacccttatacaaaa 5376
5377 ccccaaaaacaagtttcttagcaccctaccaactaaGGTACC 5418

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KpnI

FIGURE 12

Nucleotide sequence of the phaseolin promoter-caleosinGUS-phaseolin terminator sequence. The caleosinGUS coding sequence and its deduced amino acid sequence is indicated. The phaseolin promoter corresponds to nucleotide 1-1545. The sequence encoding caleosin corresponds to nt 1548-2282, the NcoI restriction, which was used for the in-frame cloning and which separates the caleosin and GUS sequence (nt 2284-2289) is underlined. The GUS sequence corresponds to nt 2286-4163. The phaseolin terminator corresponds to nucleotide sequence 4164-5384.

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1 GAATTCattgtactcccagtatcattatagtgaaagttttggctctctcgccggtgggttttttacctctattttaagggg 80
81 ttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaattatcac 160
161 gcttcgcacacgatatccctacaaattttattttgttaaacattttcaaacgcataaaattttatgaagtcctgct 240
241 atctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggtagaagcataaagattt 320
321 attcttattcttcttcatataaatgtttaatatataataaacaattctttacctaagaaggatttcccattttata 400
401 ttttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataaaattta 480
481 actccataatttttttattcgactgatcttaagcaacacccagtgacacaaactagccattttttctttgataaaaaa 560
561 atccaattatcattgtatttttttatacaatgaaaatttcaccaaacaatcatttgtgggtatttctgaagcaagtcag 640
641 ttatgcaaaattctataatttcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacatcttcta 720
721 aagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaattagat 800
801 ataattaaaaattacttttttaattttaagtttaattgttggaatttgtgactattgatttatttctactatgttta 880
881 attgttttatagatagtttaaagtaaatataagtaagttagtagagtggttagagtggtaccctaaccataaactataac 960
961 atttatgggtgactaattttcatatatttcttattgtttttaccttttcttggtatgtaagtcgtaactagaattacag 1040
1041 tgggttgccatgacactctgtggtcttttgggttcacatgcatgggtcttgcgcaagaaaaagacaaagaacaaagaaaaaag 1120
1121 acaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgctccatgtat 1200
1201 gtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatgggtcacccatctcaaccacacacacacacat 1280
1281 tgcctttttcttcatcatcaccacaaccacgttatatattcattctcttccgccacctcaatttcttcaacttcaacaca 1360
1361 cgtcaacctgcatatgcgtgtcatcccatgccccaaatctccatgcatgttccaaccaccttctctcttatataataccta 1440
1441 taaataacctctaatactactcacttctttcatcatccatccatccagagtactactactctactactataataccccaac 1520
1521 ccaactcatattcaatactactctacc ATG GGG TCA AAG ACG GAG ATG ATG GAG AGA GAC GCA ATG 1586
1      M   G   S   K   T   E   M   M   E   R   D   A   M   13
1587 GCT ACG GTG GCT CCC TAT GCG CCG GTC ACT TAC CAC CGC CGT GCT CGT GTT GAC TTG GAT 1646
14  A   T   V   A   P   Y   A   P   V   T   Y   H   R   R   A   R   V   D   L   D   33
1647 GAT AGA CTT CCT AAA CCT TAT ATG CCA AGA GCA TTG CAA GCA CCA GAC AGA GAA CAC CCG 1706
34  D   R   L   P   K   P   Y   M   P   R   A   L   Q   A   P   D   R   E   H   P   53
1707 TAC GGA ACT CCA GGC CAT AAG AAT TAC GGA CTT AGT GTT CTT CAA CAG CAT GTC TCC TTC 1766
54  Y   G   T   P   G   H   K   N   Y   G   L   S   V   L   Q   Q   H   V   S   F   73
1767 TTC GAT ATC GAT GAT AAT GGC ATC ATT TAC CCT TGG GAG ACC TAC TCT GGA CTG CGA ATG 1826
74  F   D   I   D   D   N   G   I   I   Y   P   W   E   T   Y   S   G   L   R   M   93
1827 CTT GGT TTC AAT ATC ATT GGG TCG CTT ATA ATA GCC GCT GTT ATC AAC CTG ACC CTT AGC 1886
94  L   G   F   N   I   I   G   S   L   I   I   A   A   V   I   N   L   T   L   S   113
1887 TAT GCC ACT CTT CCG GGG TGG TTA CCT TCA CCT TTC TTC CCT ATA TAC ATA CAC AAC ATA 1946
114 Y   A   T   L   P   G   W   L   P   S   P   F   F   P   I   Y   I   H   N   I   133
1947 CAC AAG TCA AAG CAT GGA AGT GAT TCA AAA ACA TAT GAC AAT GAA GGA AGG TTT ATG CCG 2006
134 H   K   S   K   H   G   S   D   S   K   T   Y   D   N   E   G   R   F   M   P   153
2007 GTG AAT CTT GAG TTG ATA TTT AGC AAA TAT GCG AAA ACC TTG CCA GAC AAG TTG AGT CTT 2066
154 V   N   L   E   L   I   F   S   K   Y   A   K   T   L   P   D   K   L   S   L   173

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FIGURE 12 (cont'd)

2067	GGA	GAA	CTA	TGG	GAG	ATG	ACA	GAA	GGA	AAC	CGT	GAC	GCT	TGG	GAC	ATT	TTT	GGA	TGG	ATC	2126
174	G	E	L	W	E	M	T	E	G	N	R	D	A	W	D	I	F	G	W	I	193
2127	GCA	GGC	AAA	ATA	GAG	TGG	GGA	CTG	TTG	TAC	TTG	CTA	GCA	AGG	GAT	GAA	GAA	GGG	TTT	TTG	2186
194	A	G	K	I	E	W	G	L	L	Y	L	L	A	R	D	E	E	G	F	L	213
2187	TCA	AAA	GAA	GCT	ATT	AGG	CGG	TGT	TTC	GAT	GGA	AGC	TTG	TTC	GAG	TAC	TGT	GCC	AAA	ATC	2246
214	S	K	E	A	I	R	R	C	F	D	G	S	L	F	E	Y	C	A	K	I	233
2247	TAC	GCT	GGT	ATC	AGT	GAA	GAC	AAG	ACA	GCA	TAC	TAC	GCC	ATG	GTC	TTA	CGT	CCT	GTA	GAA	2306
234	Y	A	G	I	S	E	D	K	T	A	Y	Y	A	M	V	L	R	P	V	E	253
2307	ACC	CCA	ACC	CGT	GAA	ATC	AAA	AAA	CTC	GAC	GGC	CTG	TGG	GCA	TTC	AGT	CTG	GAT	CGC	GAA	2366
254	T	P	T	R	E	I	K	K	L	D	G	L	W	A	F	S	L	D	R	E	273
2367	AAC	TGT	GGA	ATT	GAT	CAG	CGT	TGG	TGG	GAA	AGC	GCG	TTA	CAA	GAA	AGC	CGG	GCA	ATT	GCT	2426
274	N	C	G	I	D	Q	R	W	W	E	S	A	L	Q	E	S	R	A	I	A	293
2427	GTG	CCA	GGC	AGT	TTT	AAC	GAT	CAG	TTC	GCC	GAT	GCA	GAT	ATT	CGT	AAT	TAT	GCG	GGC	AAC	2486
294	V	P	G	S	F	N	D	Q	F	A	D	A	D	I	R	N	Y	A	G	N	313
2487	GTC	TGG	TAT	CAG	CGC	GAA	GTC	TTT	ATA	CCG	AAA	GGT	TGG	GCA	GGC	CAG	CGT	ATC	GTG	CTG	2546
314	V	W	Y	Q	R	E	V	F	I	P	K	G	W	A	G	Q	R	I	V	L	333
2547	CGT	TTC	GAT	GCG	GTC	ACT	CAT	TAC	GGC	AAA	GTG	TGG	GTC	AAT	AAT	CAG	GAA	GTG	ATG	GAG	2606
334	R	F	D	A	V	T	H	Y	G	K	V	W	V	N	N	Q	E	V	M	E	353
2607	CAT	CAG	GGC	GGC	TAT	ACG	CCA	TTT	GAA	GCC	GAT	GTC	ACG	CCG	TAT	GTT	ATT	GCC	GGG	AAA	2666
354	H	Q	G	G	Y	T	P	F	E	A	D	V	T	P	Y	V	I	A	G	K	373
2667	AGT	GTA	CGT	ATC	ACC	GTT	TGT	GTG	AAC	AAC	GAA	CTG	AAC	TGG	CAG	ACT	ATC	CCG	CCG	GGA	2726
374	S	V	R	I	T	V	C	V	N	N	E	L	N	W	Q	T	I	P	P	G	393
2727	ATG	GTG	ATT	ACC	GAC	GAA	AAC	GGC	AAG	AAA	AAG	CAG	TCT	TAC	TTC	CAT	GAT	TTC	TTT	AAC	2786
394	M	V	I	T	D	E	N	G	K	K	K	Q	S	Y	F	H	D	F	F	N	413
2787	TAT	GCC	GGA	ATC	CAT	CGC	AGC	GTA	ATG	CTC	TAC	ACC	ACG	CCG	AAC	ACC	TGG	GTG	GAC	GAT	2846
414	Y	A	G	I	H	R	S	V	M	L	Y	T	T	P	N	T	W	V	D	D	433
2847	ATC	ACC	GTG	GTG	ACG	CAT	GTC	GCG	CAA	GAC	TGT	AAC	CAC	GCG	TCT	GTT	GAC	TGG	CAG	GTG	2906
434	I	T	V	V	T	H	V	A	Q	D	C	N	H	A	S	V	D	W	Q	V	453
2907	GTG	GCC	AAT	GGT	GAT	GTC	AGC	GTT	GAA	CTG	CGT	GAT	GCG	GAT	CAA	CAG	GTG	GTT	GCA	ACT	2966
454	V	A	N	G	D	V	S	V	E	L	R	D	A	D	Q	Q	V	V	A	T	473
2967	GGA	CAA	GGC	ACT	AGC	GGG	ACT	TTG	CAA	GTG	GTG	AAT	CCG	CAC	CTC	TGG	CAA	CCG	GGT	GAA	3026
474	G	Q	G	T	S	G	T	L	Q	V	V	N	P	H	L	W	Q	P	G	E	493
3027	GGT	TAT	CTC	TAT	GAA	CTG	TGC	GTC	ACA	GCC	AAA	AGC	CAG	ACA	GAG	TGT	GAT	ATC	TAC	CCG	3086
494	G	Y	L	Y	E	L	C	V	T	A	K	S	Q	T	E	C	D	I	Y	P	513
3087	CTT	CGC	GTC	GGC	ATC	CGG	TCA	GTG	GCA	GTG	AAG	GGC	CAA	CAG	TTC	CTG	ATT	AAC	CAC	AAA	3146
514	L	R	V	G	I	R	S	V	A	V	K	G	Q	Q	F	L	I	N	H	K	533
3147	CCG	TTC	TAC	TTT	ACT	GGC	TTT	GGT	CGT	CAT	GAA	GAT	GCG	GAC	TTA	CGT	GGC	AAA	GGA	TTC	3206
534	P	F	Y	F	T	G	F	G	R	H	E	D	A	D	L	R	G	K	G	F	553
3207	GAT	AAC	GTG	CTG	ATG	GTG	CAC	GAC	CAC	GCA	TTA	ATG	GAC	TGG	ATT	GGG	GCC	AAC	TCC	TAC	3266
554	D	N	V	L	M	V	H	D	H	A	L	M	D	W	I	G	A	N	S	Y	573
3267	CGT	ACC	TCG	CAT	TAC	CCT	TAC	GCT	GAA	GAG	ATG	CTC	GAC	TGG	GCA	GAT	GAA	CAT	GGC	ATC	3326
574	R	T	S	H	Y	P	Y	A	E	E	M	L	D	W	A	D	E	H	G	I	593
3327	GTG	GTG	ATT	GAT	GAA	ACT	GCT	GCT	GTC	GGC	TTT	TCG	CTC	TCT	TTA	GGC	ATT	GGT	TTC	GAA	3386
594	V	V	I	D	E	T	A	A	V	G	F	S	L	S	L	G	I	G	F	E	613

FIGURE 12 (cont'd)

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3387 GCG GGC AAC AAG CCG AAA GAA CTG TAC AGC GAA GAG GCA GTC AAC GGG GAA ACT CAG CAA 3446
614 A G N K P K E L Y S E E A V N G E T Q Q 633
3447 GCG CAC TTA CAG GCG ATT AAA GAG CTG ATA GCG CGT GAC AAA AAC CAC CCA AGC GTG GTG 3506
634 A H L Q A I K E L I A R D K N H P S V V 653
3507 ATG TGG AGT ATT GCC AAC GAA CCG GAT ACC CGT CCG CAA GGT GCA CGG GAA TAT TTC GCG 3566
654 M W S I A N E P D T R P Q G A R E Y F A 673
3567 CCA CTG GCG GAA GCA ACG CGT AAA CTC GAC CCG ACG CGT CCG ATC ACC TGC GTC AAT GTA 3626
674 P L A E A T R K L D P T R P I T C V N V 693
3627 ATG TTC TGC GAC GCT CAC ACC GAT ACC ATC AGC GAT CTC TTT GAT GTG CTG TGC CTG AAC 3686
694 M F C D A H T D T I S D L F D V L C L N 713
3687 CGT TAT TAC GGA TGG TAT GTC CAA AGC GGC GAT TTG GAA ACG GCA GAG AAG GTA CTG GAA 3746
714 R Y Y G W Y V Q S G D L E T A E K V L E 733
3747 AAA GAA CTT CTG GCC TGG CAG GAG AAA CTG CAT CAG CCG ATT ATC ATC ACC GAA TAC GGC 3806
734 K E L L A W Q E K L H Q P I I I T E Y G 753
3807 GTG GAT ACG TTA GCC GGG CTG CAC TCA ATG TAC ACC GAC ATG TGG AGT GAA GAG TAT CAG 3866
754 V D T L A G L H S M Y T D M W S E E Y Q 773
3867 TGT GCA TGG CTG GAT ATG TAT CAC CGC GTC TTT GAT CGC GTC AGC GCC GTC GTC GGT GAA 3926
774 C A W L D M Y H R V F D R V S A V V G E 793
3927 CAG GTA TGG AAT TTC GCC GAT TTT GCG ACC TCG CAA GGC ATA TTG CGC GTT GGC GGT AAC 3986
794 Q V W N F A D F A T S Q G I L R V G G N 813
3987 AAG AAA GGG ATC TTC ACT CGC GAC CGC AAA CCG AAG TCG GCG GCT TTT CTG CTG CAA AAA 4046
814 K K G I F T R D R K P K S A A F L L Q K 833
4047 CGC TGG ACT GGC ATG AAC TTC GGT GAA AAA CCG CAG CAG GGA GGC AAA CAA TGA ATCAACAA 4108
834 R W T G M N F G E K P Q Q G G K Q * 851
4109 CTCTCCTGGCGCACCATCGTCGGCTACAGCCTCGGTGGAATTCGATATCAAGCTTaaataagtatgaactaaaatgcatg 4188
4189 taggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataataactgagctccatctcacttc 4268
4269 ttctatgaataaacaaggatgttatgatataataacactctatctatgcaccttattgttctatgataaatttcctctt 4348
4349 attattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaacaaatgtgtactataagacttt 4428
4429 ctaacaattctaaacttttagcattgtgaacgagacataagtgttaagaagacataacaattataatggaagaagtttgtc 4508
4509 tccatttatatattatattatattaccacttatgtattatattagatgttaaggagacataacaattataaagagagaagt 4588
4589 ttgtatccatttatattatataactaccatttatattataacttatccacttatttaattgtctttataaggtttgat 4668
4669 ccatgatattttctaataatttttagttgatattgtatatgaaagggactattttgaactctcttactctgtataaaggttga 4748
4749 tcatccttaaaagtgggtctattttaattttattgtcttcttacagataaaaaaaaaattatgagttggtttgataaaatatt 4828
4829 gaaggattttaaaataataaataaataaataaataacatataatataatgtatataaatttattataataacatttatctat 4908
4909 aaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaattatttaaacgagagtaaac 4988
4989 atatttgactttttggttatttaacaaattattatttaacactatatgaatttttttttttatcgggcaaggaaataaa 5068
5069 attaaattaggagggacaatgggtgtgtcccaatcctatacaaccaactccacaggaaggtcaggtcggggacaacaaa 5148
5149 aaaacaggcaagggaattttttaattttgggttgcttctgtttgtcagataatttatgcagtaaaacactacacataaccc 5228
5229 ttttagcagtagagcaatgggtgaccgtgtgcttagcttcttttattttatttttttatcagcaaagaataaataaaaata 5308
5309 aaatgagacacttcagggatgtttcaacccttatacaaaaccccaaaaacaagtttcctagcaccctaccaactaaGGTA 5388
5389 CC 5390

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FIGURE 13

Histochemical staining of β -Glucuronidase (GUS) activity in flax embryos bombarded with vectors pBluescriptIIKS+ (negative control), pSBS2098 (GUS) pSBS2037 (oleosinGUS), and pSBS2601 (caleosinGUS).

